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<110> wang, Tongwen

<120> Composistions and Methods of modulating TGF-B Signaling

<130> 17633/1082

<140> 09927738
<141> 2001-08-10

<150> US 60/119786
<151> 1999-02-11

<150> PCT/US00/03561
<151> 2000-02-11

<160> 28

<170> PatentIn version 3.1

<210> 1
<211> 277
<212> PRT
<213> Unknown

<220>
<223> Isolated using yeast two hybrid system, Clone S1 + 27

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Lys Tyr Thr Ala Phe Leu Tyr Asn Asp Gln Leu Ile Trp Ser Gly Leu

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                                    20                        25                        30

        Glu Gln Asp Asp Met Arg Ile Leu Tyr Lys Tyr Leu Thr Thr Ser Leu
                35                      40                      45

        Phe Pro Arg His Ile Glu Pro Glu Leu Ala Gly Arg Asp Ser Pro Ile
                50                      55                      60

        Arg Ala Glu Met Pro Gly Asn Leu Gln His Tyr Gly Arg Phe Leu Thr
        65                      70                      75                      80

        Gly Pro Leu Asn Leu Asn Asp Pro Asp Ala Lys Cys Arg Phe Pro Lys
                        85                      90                      95

        Ile Phe Val Asn Thr Asp Asp Thr Tyr Glu Glu Leu His Leu Ile Val
                        100                     105                     110

        Tyr Lys Ala Met Ser Ala Ala Val Cys Phe Met Ile Asp Ala Ser Val
                        115                     120                     125

        His Pro Thr Leu Asp Phe Cys Arg Arg Leu Asp Ser Ile Val Gly Pro
                130                     135                     140

        Gln Leu Thr Val Leu Ala Ser Asp Ile Cys Glu Gln Phe Asn Ile Asn
        145                     150                     155                     160

        Lys Arg Met Ser Gly Ser Glu Lys Glu Pro Gln Phe Lys Phe Ile Tyr
                        165                     170                     175

        Phe Asn His Met Asn Leu Ala Glu Lys Ser Thr Val His Met Arg Lys
                        180                     185                     190

        Thr Pro Ser Val Ser Leu Thr Ser Val His Pro Asp Leu Met Lys Ile
                        195                     200                     205

        Leu Gly Asp Ile Asn Ser Asp Phe Thr Arg Val Asp Glu Asp Glu Glu
                210                     215                     220

        Ile Ile Val Lys Ala Met Ser Asp Tyr Trp Val Val Gly Lys Lys Ser
        225                     230                     235                     240

        Asp Arg Arg Glu Leu Tyr Val Ile Leu Asn Gln Lys Asn Ala Asn Leu
                        245                     250                     255

        Ile Glu Val Asn Glu Val Lys Lys Leu Cys Ala Thr Gln Phe Asn Asn
                        260                     265                     270
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Ile Phe Phe Leu Asp
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<210> 2

<211> 543

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 28 protein

<400> 2

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Thr Gln Glu Glu Ile Ala Gln Arg Arg Glu Arg Ala Arg Gln Arg His
            20   25   30

Ala Glu Lys Leu Ala Ala Ala Gln Gly Gln Ala Pro Leu Glu Pro Thr
        35   40   45

Gln Asp Gly Ser Ala Ile Glu Thr Cys Pro Lys Gly Asp Glu Pro Arg
    50   55   60

Gly Asp Glu Gln Gln Val Glu Ser Met Thr Pro Lys Pro Val Leu Gln
65   70   75   80

Glu Glu Asn Asn Gln Glu Ser Phe Ile Ala Phe Ala Arg Val Phe Ser
            85   90   95

Gly Val Ala Arg Arg Gly Lys Lys Ile Phe Val Leu Gly Pro Lys Tyr
            100   105   110

Ser Pro Leu Glu Phe Leu Arg Arg Val Pro Leu Cys Phe Ser Ala Pro
        115   120   125

Pro Asp Gly Leu Pro Gln Val Pro His Met Ala Tyr Cys Ala Leu Glu
    130   135   140

Asn Leu Tyr Leu Leu Met Gly Arg Glu Leu Glu Tyr Leu Glu Glu Val
145   150   155   160

Pro Pro Gly Asn Val Leu Gly Ile Gly Gly Leu Gln Asp Phe Val Leu
            165   170   175

Lys Ser Ala Thr Leu Cys Ser Leu Pro Ser Cys Pro Pro Phe Ile Pro
        180   185   190

Leu Asn Phe Glu Ala Thr Pro Ile Val Arg Val Ala Val Glu Pro Lys
        195   200   205

His Pro Ser Glu Met Pro Gln Leu Val Lys Gly Met Lys Leu Leu Asn
   210   215   220

Gln Ala Asp Pro Cys Val Gln Ile Leu Ile Gln Glu Thr Gly Glu His
225   230   235   240

Val Leu Val Thr Ala Gly Glu Val His Leu Gln Arg Cys Leu Asp Asp
          245   250   255

Leu Lys Glu Arg Phe Ala Lys Ile His Ile Ser Val Ser Glu Pro Ile
         260   265   270

Ile Pro Phe Arg Glu Thr Ile Thr Lys Pro Pro Lys Val Asp Met Val
        275   280   285

Asn Glu Glu Ile Gly Lys Gln Gln Lys Val Ala Val Ile His Gln Met
     290   295   300

Lys Glu Asp Gln Ser Lys Ile Pro Glu Gly Ile Gln Val Asp Ser Asp
305   310   315   320

Gly Leu Ile Thr Ile Thr Thr Pro Asn Lys Leu Ala Thr Leu Ser Val
          325   330   335

Arg Ala Met Pro Leu Pro Glu Glu Val Thr Gln Ile Leu Glu Glu Asn
        340   345   350

Ser Asp Leu Ile Arg Ser Met Glu Gln Leu Thr Ser Ser Leu Asn Glu
        355   360   365

Gly Glu Asn Thr His Met Ile His Gln Lys Thr Gln Glu Lys Ile Trp
     370   375   380

Glu Phe Lys Gly Lys Leu Glu Gln His Leu Thr Gly Arg Arg Trp Arg
385   390   395   400

Asn Ile Val Asp Gln Ile Trp Ser Phe Gly Pro Arg Lys Cys Gly Pro
         405   410   415

Asn Ile Leu Val Asn Lys Ser Glu Asp Phe Gln Asn Ser Val Trp Thr
        420   425   430

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Gly Pro Ala Asp Lys Ala Ser Lys Glu Ala Ser Arg Tyr Arg Asp Leu
        435             440             445

Gly Asn Ser Ile Val Ser Gly Phe Gln Leu Ala Thr Leu Ser Gly Pro
    450             455             460

Met Cys Glu Glu Pro Leu Met Gly Val Cys Phe Val Leu Glu Lys Trp
465             470             475             480

Asp Leu Ser Lys Phe Glu Glu Gln Gly Ala Ser Asp Leu Ala Lys Glu
            485             490             495

Asp Arg Arg Lys Met Lys Pro Val Leu Val Glu Met Lys Thr Lys Ser
            500             505             510

Tyr Lys Met Ala Ala Leu Arg Pro Leu Arg Arg Gly His His Arg Lys
        515             520             525

Glu Asn Leu His Ser Leu Thr Ala Met Asp Leu Ser Gln Asp Ser
    530             535             540
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<210> 3

<211> 396

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 19

<400> 3

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Arg Asp Gly Asp Val Val Leu Pro Ala Gly Val Val Val Lys Gln Glu
            20              25              30

Arg Leu Ser Pro Glu Val Ala Pro Pro Ala His Arg Arg Pro Asp His
        35              40              45

Ser Gly Gly Ser Pro Ser Pro Pro Thr Ser Glu Pro Ala Arg Ser Gly
    50              55              60

His Arg Gly Asn Arg Ala Arg Gly Val Ser Arg Ser Pro Pro Lys Lys
```

65   70   75   80

Lys Asn Lys Ala Ser Gly Arg Arg Ser Lys Ser Pro Arg Ser Lys Arg
                85   90   95

Asn Arg Ser Pro His His Ser Thr Val Lys Val Lys Gln Glu Arg Glu
            100   105   110

Asp His Pro Arg Arg Gly Arg Glu Asp Arg Gln His Arg Glu Pro Ser
            115   120   125

Glu Gln Glu His Arg Arg Ala Arg Asn Ser Asp Arg Asp Arg His Arg
        130   135   140

Gly His Ser His Gln Arg Arg Thr Ser Asn Glu Arg Pro Gly Ser Gly
145   150   155   160

Gln Gly Gln Gly Arg Asp Arg Asp Thr Gln Asn Leu Gln Ala Gln Glu
                165   170   175

Glu Glu Arg Glu Phe Tyr Asn Ala Arg Arg Arg Glu His Arg Gln Arg
            180   185   190

Asn Asp Val Gly Gly Gly Gly Ser Glu Ser Gln Glu Leu Val Pro Arg
            195   200   205

Pro Gly Gly Asn Asn Lys Glu Lys Glu Val Pro Ala Lys Glu Lys Pro
    210   215   220

Ser Phe Glu Leu Ser Gly Ala Leu Leu Glu Asp Thr Asn Thr Phe Arg
225   230   235   240

Gly Val Val Ile Lys Tyr Ser Glu Pro Pro Glu Ala Arg Ile Pro Lys
                245   250   255

Lys Arg Trp Arg Leu Tyr Pro Phe Lys Asn Asp Glu Val Leu Pro Val
            260   265   270

Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg His Arg Arg
            275   280   285

Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys Gln His Ala
    290   295   300

Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp Gly Thr Val
305   310   315   320

Page 6

```
Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser Gly Asn Gly
                325             330             335

Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr Tyr Glu Leu
            340             345             350

Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg Glu Tyr Val
            355             360             365

Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg Lys Asp Asp
    370             375             380

Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser
385             390             395
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<210> 4

<211> 82

<212> PRT

<213> Unknown

<220>

<223> Protein Sequence of NIPP-1 domain homologous to SNIP 1

<400> 4

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1           5               10              15

Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His Lys His Leu
            20              25              30

Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly Thr Phe Leu
            35              40              45

Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile Pro Ile Asp
    50              55              60

Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr Leu Arg Glu
65              70              75              80

Lys Pro
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<210> 5

<211> 255
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<212>    PRT

<213>    Unknown


<220>

<223>    Clone S1 + 19 Smad binding domain sequence

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Arg His Arg Gly His Ser His Gln Arg Arg Thr Ser Asn Glu Arg Pro
1           5               10              15

Gly Ser Gly Gln Gly Gln Gly Arg Asp Arg Asp Thr Gln Asn Leu Gln
        20              25              30

Ala Gln Glu Glu Glu Arg Glu Phe Tyr Asn Ala Arg Arg Arg Glu His
        35              40              45

Arg Gln Arg Asn Asp Val Gly Gly Gly Ser Glu Ser Gln Glu Leu
    50              55              60

Val Pro Arg Pro Gly Gly Asn Asn Lys Glu Lys Glu Val Pro Ala Lys
65              70              75              80

Glu Lys Pro Ser Phe Glu Leu Ser Gly Ala Leu Leu Glu Asp Thr Asn
        85              90              95

Thr Phe Arg Gly Val Val Ile Lys Tyr Ser Glu Pro Pro Glu Ala Arg
        100             105             110

Ile Pro Lys Lys Arg Trp Arg Leu Tyr Pro Phe Lys Asn Asp Glu Val
        115             120             125

Leu Pro Val Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg
    130             135             140

His Arg Arg Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys
145             150             155             160

Gln His Ala Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp
            165             170             175

Gly Thr Val Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser
        180             185             190

Gly Asn Gly Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr
    195             200             205

Tyr Glu Leu Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg
210                  215                  220

Glu Tyr Val Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg
225              230                  235                  240

Lys Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser
                245                  250                  255

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<211>  163

<212>  PRT

<213>  Unknown


<220>

<223>  clone S1 +19 protein

<400>  6

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Tyr Asn Glu Pro Pro Glu Ala Lys Lys Pro Asn Ala Arg Trp Arg Leu
              20                  25                  30

Tyr Pro Phe Lys Gly Glu Glu Ser Leu Gln Val Leu Tyr Ile His Arg
          35                  40                  45

Gln Ser Ala Tyr Leu Ile Gly Arg Asp His Lys Ile Ala Asp Ile Pro
      50                  55                  60

Val Asp His Pro Ser Cys Ser Lys Gln His Ala Val Leu Gln Phe Arg
65                  70                  75                  80

Ser Met Pro Phe Thr Arg Asp Asp Gly Thr Lys Ala Arg Arg Ile Met
                  85                  90                  95

Pro Tyr Ile Ile Asp Leu Gly Ser Gly Asn Gly Thr Phe Leu Asn Glu
              100                 105                 110

Lys Lys Ile Glu Pro Gln Arg Tyr Ile Glu Leu Gln Glu Lys Asp Met
          115                 120                 125

Leu Lys Phe Gly Phe Ser Thr Arg Glu Tyr Val Val Met Lys Glu Arg

                130                           135                          140

Glu Ile Thr Glu Glu Glu Leu Ala Glu Gly Glu Asp Val Lys Lys Glu
145                     150                     155                     160

Glu Ser Asp


<210> 7

<211> 198

<212> PRT

<213> Unknown


<220>

<223> Clone S1 + 12 Protein

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Glu Phe Gly Thr Arg Arg Met Met Glu Gly Leu Asp Asp Gly Pro Asp
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Phe Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu
            20                      25                      30


Gln Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu
            35                      40                      45


Arg Asp Lys Val Lys Phe Thr Val His Thr Lys Ser Ser Leu Pro Asn
        50                      55                      60


Phe Lys Gln Asn Glu Phe Ser Val Val Arg Gln His Glu Glu Phe Ile
65                      70                      75                      80


Trp Leu His Asp Ser Phe Val Glu Asn Glu Asp Tyr Ala Gly Tyr Ile
                85                      90                      95


Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys
                100                     105                     110


Leu Gln Lys Leu Gly Glu Gly Glu Gly Ser Met Thr Lys Glu Glu Phe
            115                     120                     125


Thr Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys
            130                     135                     140

Lys Thr Val Ala Met His Glu Val Phe Leu Cys Arg Val Ala Ala His
145            150             155                 160

Pro Ile Leu Arg Arg Asp Leu Asn Phe His Val Phe Leu Glu Tyr Asn
                165             170             175

Gln Asp Leu Ser Val Arg Gly Lys Lys Lys Lys Asn Ser Arg Ser
            180             185             190

Phe Gly Leu Leu Arg Gln
            195

<210>   8

<211>   414

<212>   PRT

<213>   Unknown


<220>

<223>   Clone S1+12 -2 protein Sequence

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His Ala Ser Gly Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly
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Pro Asp Phe Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val
                20              25              30

Asp Leu Gln Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu
            35              40              45

Ser Glu Arg Asp Lys Val Lys Phe Thr Val His Thr Lys Ser Ser Leu
        50              55              60

Pro Asn Phe Lys Gln Asn Glu Phe Ser Val Val Arg Gln His Glu Glu
65              70              75                  80

Phe Ile Trp Leu His Asp Ser Phe Val Glu Asn Glu Asp Tyr Ala Gly
                85              90              95

Tyr Ile Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Asp Ala Ser Arg
                100             105             110

Glu Lys Leu Gln Lys Leu Gly Glu Gly Glu Gly Ser Met Thr Lys Glu
            115             120             125

```
Glu Phe Thr Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu Ala Ile
    130             135             140

Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Cys Arg Val Ala
145             150             155             160

Ala His Pro Ile Leu Arg Arg Asp Leu Asn Phe His Val Phe Leu Glu
            165             170             175

Tyr Asn Gln Asp Leu Ser Val Arg Gly Lys Asn Lys Lys Glu Lys Leu
            180             185             190

Glu Asp Phe Phe Lys Asn Met Val Lys Ser Ala Asp Gly Val Ile Val
            195             200             205

Ser Gly Val Lys Asp Val Asp Asp Phe Phe Glu His Glu Arg Thr Phe
    210             215             220

Leu Leu Glu Tyr His Asn Arg Val Lys Asp Ala Ser Ala Lys Ser Asp
225             230             235             240

Arg Met Thr Arg Ser His Lys Ser Ala Ala Asp Asp Tyr Asn Arg Ile
            245             250             255

Gly Ser Ser Leu Tyr Ala Leu Gly Thr Gln Asp Ser Thr Asp Ile Cys
            260             265             270

Lys Phe Phe Leu Lys Val Ser Glu Leu Phe Asp Lys Thr Arg Lys Ile
            275             280             285

Glu Ala Arg Val Ser Ala Asp Glu Asp Leu Lys Leu Ser Asp Leu Leu
    290             295             300

Lys Tyr Tyr Leu Arg Glu Ser Gln Ala Ala Lys Asp Leu Leu Tyr Arg
305             310             315             320

Arg Ser Arg Ser Leu Val Asp Tyr Glu Asn Ala Asn Lys Ala Leu Asp
            325             330             335

Lys Ala Arg Ala Lys Asn Lys Asp Val Leu Gln Ala Glu Thr Ser Gln
            340             345             350

Gln Leu Cys Cys Gln Lys Phe Glu Lys Ile Ser Glu Ser Ala Lys Gln
            355             360             365

Glu Leu Ile Asp Phe Lys Thr Arg Arg Val Ala Ala Phe Arg Lys Asn
    370             375             380
```

Leu Val Glu Leu Ala Glu Leu Glu Leu Lys His Ala Lys Gly Asn Leu
385   390   395   400

Gln Leu Leu Gln Asn Cys Leu Ala Val Leu Asn Gly Asp Thr
                405   410

<210>   9

<211>   294

<212>   PRT

<213>   Unknown

<220>

<223>   Clone S1+12 -5 protein

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1   5   10   15

Val Cys Cys Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His
            20   25   30

Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp
            35   40   45

Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg
        50   55   60

Gly Lys Asn Lys Lys Glu Lys Leu Glu Asp Phe Phe Lys Asn Met Val
65   70   75   80

Lys Ser Ala Asp Gly Val Ile Val Ser Gly Val Lys Asp Val Asp Asp
                85   90   95

Phe Phe Glu His Glu Arg Thr Phe Leu Leu Glu Tyr His Asn Arg Val
                100   105   110

Lys Asp Ala Ser Ala Lys Ser Asp Arg Met Thr Arg Ser His Lys Ser
            115   120   125

Ala Ala Asp Asp Tyr Asn Arg Ile Gly Ser Ser Leu Tyr Ala Leu Gly
        130   135   140

Thr Gln Asp Ser Thr Asp Ile Cys Lys Phe Phe Leu Lys Val Ser Glu
                                        Page 13

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     145                150                155                160

Leu Phe Asp Lys Thr Arg Lys Ile Glu Ala Arg Val Ser Ala Asp Glu
             165             170             175

Asp Leu Lys Leu Ser Asp Leu Leu Lys Tyr Tyr Leu Arg Glu Ser Gln
             180             185             190

Ala Ala Lys Asp Leu Leu Tyr Arg Arg Ser Arg Ser Leu Val Asp Tyr
             195             200             205

Glu Asn Ala Asn Lys Ala Leu Asp Lys Ala Arg Ala Lys Asn Lys Asp
     210             215             220

Val Leu Gln Ala Glu Thr Ser Gln Gln Leu Cys Cys Gln Lys Phe Glu
225             230             235             240

Lys Ile Ser Glu Ser Ala Lys Gln Glu Leu Ile Asp Phe Lys Thr Arg
             245             250             255

Arg Val Ala Ala Phe Arg Lys Asn Leu Val Glu Leu Ala Glu Leu Glu
             260             265             270

Leu Lys His Ala Lys Gly Asn Leu Gln Leu Leu Gln Asn Cys Leu Ala
             275             280             285

Val Leu Asn Gly Asp Thr
     290
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<210> 10

<211> 989

<212> DNA

<213> Unknown

<220>

<223> Clone S3-1 DNA Sequence. Called tumor associated gene in homo sap
iens, unknown function

<220>

<221> misc_feature

<222> (1)..(989)

<223> n can be any nucleotide

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aatggtgctt caattggatg tgttgcaccc cgatgtaaac gaagttatca tttcccatgt     180

ggacttcaga gagaatgtat tttccagttt actggcaatt ttgcgtcatt ttgttgggac     240

catcgacctg ttcaaataat tacatctaat aattatagag agtccttacc atgcaccatt     300

tgcttggaat ttattgagcc tattccaagt tataacatat tacgaagtcc ttgttgtaag     360

aacgcttggt ttcatagaga ctgtttacag gttcaagcaa taaatgcggg agtgtttttc     420

tttaggtgta caatatgcaa taatagtgac atctttcaga aagagatgtt gagaatggga     480

attcatattc ctgaaaaaga tgcttcctgg gaattagagg aaaacgctta tcaagagctt     540

ctgcagcact atgagcgttg tgatgttcga agatgtcgtt gcaaagaagg gcgagactat     600

aatgcacctg atagcaaatg ggaaataaag cgctgtcagt gttgtggttc cagtggcaca     660

catttagcct gctcctcatt acggtcatgg gagcaaaatt gggagtgttt ggaatgtagg     720

ggtattatct acaattcagg agagttccaa acagccaaaa aacatgtatt acccaattct     780

aataatgtgg ggattacaga ttgtttgttg gaagagtcat cacctaaatt acccagacag     840

tcacctggat cccagagtaa agatctactg aggcaaggca gcaaatttag aagaaatgta     900

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<210> 11

<211> 329

<212> PRT

<213> Unknown

<220>

<223>   Clone S3-1 protein Sequence

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<221> MISC_FEATURE

<222> (1)..(329)

<223> X can be any amino acid

<400> 11

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1             5             10                      15

Gly Phe Leu Ile Glu Asp Ile Arg Lys Glu Val Asn Arg Ala Ser Lys
            20              25                30

Leu Lys Cys Cys Val Cys Lys Lys Asn Gly Ala Ser Ile Gly Cys Val
        35              40              45

Ala Pro Arg Cys Lys Arg Ser Tyr His Phe Pro Cys Gly Leu Gln Arg
    50              55                  60

Glu Cys Ile Phe Gln Phe Thr Gly Asn Phe Ala Ser Phe Cys Trp Asp
65              70                  75                  80

His Arg Pro Val Gln Ile Ile Thr Ser Asn Asn Tyr Arg Glu Ser Leu
                85              90                  95

Pro Cys Thr Ile Cys Leu Glu Phe Ile Glu Pro Ile Pro Ser Tyr Asn
            100             105                 110

Ile Leu Arg Ser Pro Cys Cys Lys Asn Ala Trp Phe His Arg Asp Cys
        115             120                 125

Leu Gln Val Gln Ala Ile Asn Ala Gly Val Phe Phe Phe Arg Cys Thr
    130             135                 140

Ile Cys Asn Asn Ser Asp Ile Phe Gln Lys Glu Met Leu Arg Met Gly
145             150                 155                 160

Ile His Ile Pro Glu Lys Asp Ala Ser Trp Glu Leu Glu Glu Asn Ala
            165                 170                 175

Tyr Gln Glu Leu Leu Gln His Tyr Glu Arg Cys Asp Val Arg Arg Cys
        180                 185                 190

Arg Cys Lys Glu Gly Arg Asp Tyr Asn Ala Pro Asp Ser Lys Trp Glu
        195                 200                 205

Ile Lys Arg Cys Gln Cys Cys Gly Ser Ser Gly Thr His Leu Ala Cys
    210             215                 220

Ser Ser Leu Arg Ser Trp Glu Gln Asn Trp Glu Cys Leu Glu Cys Arg
225             230                 235                 240

Gly Ile Ile Tyr Asn Ser Gly Glu Phe Gln Thr Ala Lys Lys His Val
            245                 250                 255
```

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Leu Pro Asn Ser Asn Asn Val Gly Ile Thr Asp Cys Leu Leu Glu Glu
            260             265             270

Ser Ser Pro Lys Leu Pro Arg Gln Ser Pro Gly Ser Gln Ser Lys Asp
            275             280             285

Leu Leu Arg Gln Gly Ser Lys Phe Arg Arg Asn Val Ser Thr Leu Leu
            290             295             300

Ile Glu Leu Gly Phe Gln Ile Lys Lys Lys Lys Lys Leu Glu Lys
305             310             315             320

Xaa Gly Xaa Phe Ala Arg Gly Leu Val
            325
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<210> 12

<211> 1673

<212> DNA

<213> Unknown

<220>

<223> Clone S3-12 DNA sequence

<400> 12

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catcaggcca gaggaatgag cctgcagtca aattaccttg gactagcggc agcacctgca   240
attatgagtt atgcagaatg ttctgtccca attggagtga ctgctccctc attgcagcca   300
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gaatcaactg cacagaagcg aattgaagag tggaaacagc agcagctggt tagtggcatg   600
gcagagagaa atgctaattt tgaagccctt cctgaggatt ggagagcaag gctgaagaga   660
aggaaaatgg ctccaaacac atagttttta agttttaaa acttttttgt attattgttt   720
gttttgtgtt cagttcaaag tcttaaccag ttttattgtc aaataaacta taaatgttat   780
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attaacttct cctccagaac aagtgcaatt cagaaggcag ctctgcattc taccttgctt   1080

gactggaatt gtctgaagct ttttctggcc tcttttctct agtcggccac ccctgaagtg   1140

ctgaggtcta agtggtttac ctcgtgctga tagatggcca cactctttag agtagttctc   1200

ataagttcta gaactggtag ctcggtcgtt tcgcacacta ggtggcatac aggcagcagc   1260

aggtgttcat atccttgatt ttgagaattt cccctcaagt atgtggcagt aaatacaaca   1320

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attgtgtttt aaagctcttt gtatttctcc agtttctgac cttgtaaatt tgtatatatg   1560

cactaataaa gcttttttta taatcctgaa aaaaaaaaaa aaaaaaaaaa aaaactcgag   1620

aagctttgga cttcttcgcc agaggtttgg tcaagtctcc aatcaaggtt gtc          1673
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<210> 13

<211> 233

<212> PRT

<213> Unknown

<220>

<223> Clone S3 +12 protein

<400> 13

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Glu Phe Gly Thr Arg Arg Arg Lys Ala Thr Glu Ile Ser Thr Ala Val
1               5                  10                  15


Val Gln Arg Ser Ala Thr Ile Gly Ser Ser Pro Val Leu Tyr Ser Gln
                20                  25                  30


Ser Ala Ile Ala Thr Gly His Gln Ala Ala Gly Ile Gly Asn Gln Ala
            35                  40                  45


Thr Gly Ile Gly His Gln Thr Ile Pro Val Ser Leu Pro Ala Ala Gly
        50                  55                  60


Met Gly His Gln Ala Arg Gly Met Ser Leu Gln Ser Asn Tyr Leu Gly
```

```
         65                      70                      75                      80

Leu Ala Ala Ala Pro Ala Ile Met Ser Tyr Ala Glu Cys Ser Val Pro
                85                  90                  95

Ile Gly Val Thr Ala Pro Ser Leu Gln Pro Val Gln Ala Arg Gly Ala
               100             105             110

Val Pro Thr Ala Thr Ile Ile Glu Pro Pro Pro Pro Pro Pro Pro Pro
           115                 120                 125

Pro Pro Pro Pro Pro Pro Ala Pro Lys Met Pro Pro Pro Glu Lys Thr
       130                 135                 140

Lys Lys Gly Arg Lys Asp Lys Ala Lys Lys Ser Lys Thr Lys Met Pro
145                 150                 155                 160

Ser Leu Val Lys Lys Trp Gln Ser Ile Gln Arg Glu Leu Asp Glu Glu
               165                 170                 175

Asp Asn Ser Ser Ser Ser Glu Glu Asp Arg Glu Ser Thr Ala Gln Lys
               180                 185                 190

Arg Ile Glu Glu Trp Lys Gln Gln Gln Leu Val Ser Gly Met Ala Glu
           195                 200                 205

Arg Asn Ala Asn Phe Glu Ala Leu Pro Glu Asp Trp Arg Ala Arg Leu
    210                 215                 220

Lys Arg Arg Lys Met Ala Pro Asn Thr
225                 230
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<210> 14

<211> 926

<212> DNA

<213> Unknown

<220>

<223>   Clone S3 + 103 DNA sequence

<400>   14
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gaattcggca cgaggcggac gtcattgagc tgcgaccctt gttcaacgcc gttgggcaag        60

ccagctgctg gaggtgccga gaatctgagt ttcggcaagc agccaggtct ggaaactaat       120

attttaaaaa tgactacacc aaacaagaca cctcctggtg ctgaccccaa gcagttggaa       180
```

```
aggactggaa cagtacggga aattgggtca caagctgttt ggtcactctc atcttgcaaa    240

ccaggatttg gagtggatca gttacgagat gacaatctag aaacttattg gcaatcagat    300

ggttcccagc ctcatttagt gaacatccaa ttcagaagaa aaacaacagt gaagacatta    360

tgtatttatg cagactacaa atctgatgaa agctatactc caagcaagat ctcagtcaga    420

gtaggaaata attttcacaa ccttcaagaa attcggcaac ttgagttggt ggaaccaagt    480

ggctggattc atgttccctt aactgacaat cataagaagc caactcgtac attcatgata    540

cagattgctg ttctagccaa tcaccagaat ggaagagaca cccatatgag acaaattaaa    600

atatacacac cagtagaaga gagctccatt ggtaaatttc ctagatgtac aactatagat    660

ttcatgatgt atcgttcaat aaggtgactt taaaatgaga cgaaaatcat taaacgtatc    720

tttgttctta tcctgtattt aaataatata tcatgtacct ttattgaaca aggcatccgt    780

tatatctaat tttgtatatg tttaaaaata ttttattgta actttgacaa ataaatttgg    840

ggtcatatta tctttatttt ctttaacatg taataaagct cacatatttt acattaaaaa    900

aaaaaaaaaa aaaaaaactc gagaag                                          926
```

<210>   15

<211>   301

<212>   PRT

<213>   Unknown

<220>

<223>   Clone S3 + 103 prtoein Sequence

<400>   15

```
Glu Phe Gly Thr Arg Arg Thr Ser Leu Ser Cys Asp Pro Cys Ser Thr
1               5                   10                  15


Pro Leu Gly Lys Pro Ala Ala Gly Gly Ala Glu Asn Leu Ser Phe Gly
                20                  25                  30


Lys Gln Pro Gly Leu Glu Thr Asn Ile Leu Lys Met Thr Thr Pro Asn
                35                  40                  45


Lys Thr Pro Pro Gly Ala Asp Pro Lys Gln Leu Glu Arg Thr Gly Thr
        50                  55                  60


Val Arg Glu Ile Gly Ser Gln Ala Val Trp Ser Leu Ser Ser Cys Lys
65                  70                  75                  80
```

Pro Gly Phe Gly Val Asp Gln Leu Arg Asp Asp Asn Leu Glu Thr Tyr
                   85   90   95

Trp Gln Ser Asp Gly Ser Gln Pro His Leu Val Asn Ile Gln Phe Arg
            100   105   110

Arg Lys Thr Thr Val Lys Thr Leu Cys Ile Tyr Ala Asp Tyr Lys Ser
            115   120   125

Asp Glu Ser Tyr Thr Pro Ser Lys Ile Ser Val Arg Val Gly Asn Asn
        130   135   140

Phe His Asn Leu Gln Glu Ile Arg Gln Leu Glu Leu Val Glu Pro Ser
145   150   155   160

Gly Trp Ile His Val Pro Leu Thr Asp Asn His Lys Lys Pro Thr Arg
                165   170   175

Thr Phe Met Ile Gln Ile Ala Val Leu Ala Asn His Gln Asn Gly Arg
                180   185   190

Asp Thr His Met Arg Gln Ile Lys Ile Tyr Thr Pro Val Glu Glu Ser
        195   200   205

Ser Ile Gly Lys Phe Pro Arg Cys Thr Thr Ile Asp Phe Met Met Tyr
    210   215   220

Arg Ser Ile Arg Leu Asn Glu Thr Lys Ile Ile Lys Arg Ile Phe Val
225   230   235   240

Leu Ile Leu Tyr Leu Asn Asn Ile Ser Cys Thr Phe Ile Glu Gln Gly
            245   250   255

Ile Arg Tyr Ile Phe Cys Ile Cys Leu Lys Ile Phe Tyr Cys Asn Phe
            260   265   270

Asp Lys Ile Trp Gly His Ile Ile Phe Ile Phe Phe Asn Met Ser Ser
        275   280   285

His Ile Leu His Lys Lys Lys Lys Lys Lys Asn Ser Arg
    290   295   300

<210>   16

<211>   844

<212>   DNA

<213>   Unknown

<220>

<223>   Clone S3 + 125 DNA Sequence

<220>

<221>   misc_feature

<222>   (1)..(844)

<223>   n Can be any nucleotide

<400>   16

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caggaatctg tccgaagata attgaggcag aagagtccag aatgggcctc atcatcgtca      60
atgcctggta cgggaacttt gtcaatgaca agagcaggaa gagcgagaag gtgaaggtga     120
ttgacgtgac tgtgccctgc agtgcctggg taaggactcg aagctcatcc tcacgaggcc     180
tccaagctgg gctgcctggc ttttatgacc cgtgtgtggg ggaagagaag aacctgaaag     240
tgctctatca gttccggggc gtcctgcatc aggtgatggt gctggacagt gaggccctcc     300
ggataccaaa gcagtcccac aggatcgata cagatggata aactgccaag aaccagattt     360
ttaaaaggcc gcaaaaaatc ttttcctggg agtctacaaa tttggaaatg aaaaaaccca     420
gacatcagat gtttttattt tatattatta ttatagaagg tggtaccatt atcaattatg     480
tgaagggaca tgcagacacc ccagcactgg tatctgagta acggctaaga acctccttcc     540
tctggttttg aaaagcagtt cgggttgtcc aattctgtaa cattcatctc cattttttaa     600
aaaggtttct ctgacggccc cacggcccga gccgcggtga gcgtcgtgtt gcatgagcct     660
gggccccggg cttcccgtgc gcctctgccg caggtgcttc tgggcaccca tcctctgcgt     720
ttcatttgca gtcgactgta cagaaggcac tcaccacaat aaacctttcc tgaaagcaaa     780
aaaaaaaaaa aaaaaactcg agaaggtttg gacttgttcg ccagaggttt ggtcaagtnt     840
ccaa                                                                 844
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<210>   17

<211>   118

<212>   PRT

<213>   Unknown

<220>

<223>   Clone S3 + 125 Protein Sequence

<400> 17

Ile Arg His Glu Ala Ala Gly Ile Cys Pro Lys Ile Ile Glu Ala Glu
1   5   10   15

Glu Ser Arg Met Gly Leu Ile Ile Val Asn Ala Trp Tyr Gly Asn Phe
                20   25   30

Val Asn Asp Lys Ser Arg Lys Ser Glu Lys Val Lys Val Ile Asp Val
            35   40   45

Thr Val Pro Cys Ser Ala Trp Val Arg Thr Arg Ser Ser Ser Ser Arg
        50   55   60

Gly Leu Gln Ala Gly Leu Pro Gly Phe Tyr Asp Pro Cys Val Gly Glu
65   70   75   80

Glu Lys Asn Leu Lys Val Leu Tyr Gln Phe Arg Gly Val Leu His Gln
                85   90   95

Val Met Val Leu Asp Ser Glu Ala Leu Arg Ile Pro Lys Gln Ser His
                100   105   110

Arg Ile Asp Thr Asp Gly
                115

<210> 18

<211> 216

<212> DNA

<213> Unknown

<220>

<223> Clone S1 + 30 DNA Sequence

<400> 18
gaattcggca cgaggcggac aaagggaatc aaagttgtgg gaaaatggaa ggaagtgaag   60

attgacccaa atatgtttgc agatggacag atggatgact tggtgtgctt tgaggaattg   120

acagattacc agttggtctc ccctgccaag aattccctcc agctctcttc tcaaaggaag   180

cacccaagag aaaggcacaa gctgtttcag aagaag   216

<210> 19

<211> 72

<212> PRT

<213> Unknown

<220>

<223> Clone S1 + 30 Protein Sequence

<400> 19

```
Glu Phe Gly Thr Arg Arg Thr Lys Gly Ile Lys Val Val Gly Lys Trp
1               5                   10                  15


Lys Glu Val Lys Ile Asp Pro Asn Met Phe Ala Asp Gly Gln Met Asp
                20                  25                  30


Asp Leu Val Cys Phe Glu Glu Leu Thr Asp Tyr Gln Leu Val Ser Pro
            35                  40                  45


Ala Lys Asn Ser Leu Gln Leu Ser Ser Gln Arg Lys His Pro Arg Glu
        50                  55                  60


Arg His Lys Leu Phe Gln Lys Lys
65                  70
```

<210> 20

<211> 261

<212> DNA

<213> Unknown

<220>

<223> Clone S3+14 5' DNA sequence

<400> 20

```
cgatttctag cgtatatgga ggatcgcaga aaacagaagt ggcaaagatg taaaaaaaat        60
aataaggcag aattgaactg tttgggaatg gaaccagtac agacagctaa ctctagaaat       120
gggaaaaagg gtcatcacac tgaaacggtg ttcaaccggg ttttgccagg gcctattgca       180
ccagagagca gcaagaagcg gcccgtagat gcgaccagac ctttctaaga tgatggccct       240
catgcaggtg gaagcatcgg t                                                 261
```

<210> 21

<211> 547

<212> DNA

<213> Unknown

<220>

<223> Clone S3+14 3' DNA sequence

<400> 21

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agaggccctc atgcagggtg gaagcactgg gtctctatct ctgcataaca cgttccaaca    60
cagcagtagt ggcctacagt ctgtgtcatc tttgggtcac agcagtgcca cttctgcatc   120
tttgcctttt atgccatttg tgatgggtgg tgcaccatca tcccctcatg tagactccag   180
caccatgctt catcaccacc accaccaccc ccacccccac catcaccacc atcaccatcc   240
aggcttgaga gcccctggct acccctcttc accagtgact accgcctctg gtactacctt   300
gcggttgcca ccactgcaac ctgaggagga tgacgatgag gatgaagaag atgatgatga   360
cttatctcag ggctatgata gctcagaaag ggacttctca ctcattgatg atcctatgat   420
gccagctaac tcagactcca gtgaagatgc tgatgactga agccccagca tgggcccat    480
tgcttgggcg gctgctgtat tttcatttac tctggccctt ggactatgga aacgtgggag   540
gggcagg                                                              547
```

<210> 22

<211> 152

<212> PRT

<213> Unknown

<220>

<223> Clone S3+14 protein sequence

<400> 22

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Glu Ala Leu Met Gln Gly Gly Ser Thr Gly Ser Leu Ser Leu His Asn
1               5                   10                  15


Thr Phe Gln His Ser Ser Ser Gly Leu Gln Ser Val Ser Ser Leu Gly
                20                  25                  30


His Ser Ser Ala Thr Ser Ala Ser Leu Pro Phe Met Pro Phe Val Met
            35                  40                  45


Gly Gly Ala Pro Ser Ser Pro His Val Asp Ser Ser Thr Met Leu His
        50                  55                  60
```

```
His His His His His Pro His Pro His His His His His His His Pro
65              70          75              80
```

```
Gly Leu Arg Ala Pro Gly Tyr Pro Ser Ser Pro Val Thr Thr Ala Ser
                85          90              95
```

```
Gly Thr Thr Leu Arg Leu Pro Pro Leu Gln Pro Glu Glu Asp Asp Asp
            100         105         110
```

```
Glu Asp Glu Glu Asp Asp Asp Asp Leu Ser Gln Gly Tyr Asp Ser Ser
        115         120         125
```

```
Glu Arg Asp Phe Ser Leu Ile Asp Asp Pro Met Met Pro Ala Asn Ser
    130         135         140
```

```
Asp Ser Ser Glu Asp Ala Asp Asp
145         150
```

<210>   23

<211>   2496

<212>   DNA

<213>   Unknown

<220>

<223>   Clone s1+19 cDNA sequence

<400>   23

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agagcgaacg ggagcgaggg agccggcgaa gacaccggga cggggacgtg gtgctgccgg     120

cggggggtggt ggtgaagcag gagcgtctca gcccagaagt cgcacctccc gcccaccgcc    180

gtccggacca ctccggtggt agcccgtctc cgccgaccag cgagccggcc cgctcgggcc     240

accgcgggaa ccgagcccga ggagttagcc ggtccccacc caaaaagaaa acaaggcct      300

cagggagaag aagcaagtct cctcgcagta agagaaaccg aagtcctcac cactcaacag     360

tcaaagtgaa gcaggagcgt gaggatcatc cccggagagg acgggaggat cggcagcaca     420

gggaaccatc agaacaggaa cacaggagag ctaggaacag tgaccgggac agacaccggg     480

gccattccca ccaaaggaga acgtctaacg agaggcctgg gagtgggcag ggtcagggac     540

gggatcgaga cactcagaac ctgcaggctc aggaagaaga gcgggagttt tataatgcca     600

ggcgacggga gcatcgccag aggaatgacg ttggtggtgg cggcagtgag tctcaggagt     660

tggttcctcg gcctggtggc aacaacaaag aaaaagaggt gcccgctaaa gaaaaaccaa     720
```

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```
gctttgaact ttctgggggca cttcttgagg acaccaacac tttccggggt gtagtcatta    780

aatatagtga gccccccagaa gcacgtatcc ccaaaaaacg gtggcgtctc tacccattta    840

aaaatgatga ggtgcttcca gtcatgtaca tacatcgaca gagtgcgtac ctactgggtc    900

gacaccgccg cattgcagac attccaattg atcacccgtc ttgttcaaag cagcatgcgg    960

tctttcaata tcggcttgtg gaatataccc gtgctgatgg cacagttggc cgaagagtga   1020

agccctacat cattgacctt ggctcaggca atggaacctt cttaaacaac aaacgtattg   1080

agccacagag atactatgaa ctaaaagaaa aggatgtact caaatttgga ttcagtagca   1140

gagaatacgt cttgctccat gagtcgtcgg acacttctga aatagacagg aaagatgacg   1200

aggatgagga ggaggaggaa gaagtgtctg acagctagca aactaagaac ccaaactatt   1260

gatacacggt ttccttcttg gaagtctttg attgactcag agagcactat ggtggtgggt   1320

ccagcactat ggtgctctct gtaatgcctc ttactgcctt aagtctttcc tctgttgctg   1380

accagattgt gttaccattt gaatacactg actaatgttt gttaaacttt ttctgtggca   1440

ccttggccac atgcctgcag gcatttgttt tcagaacagt ctcaccaatt acaacacacc   1500

gtgttttagt agaagtgttg tggtttttagt tggtgctttc agaactgctg cctaggaaac   1560

tataaacct tggttaaggg gaaatcatgg cttgttctct ttgtacagtt actttatta    1620

tataggtgtt aagctttgtg gaccaggtgt ttttctttg gggcgaaccc ctgagcagag   1680

aatcttacta ggctttggtt atcaccaaaa caacctccag tatataccaa agctttgact   1740

tgtttgagct cttgagctta gaagttgatt ttgcacttat tttttgggg ggtgggaatg   1800

tactgcagtc agtaaacatt attgactgtt taacttaaac agatgcttta tggcacctgc   1860

tcaagcccgt gactgtacag aaggatcctg gttgctacca gtgggtgctg attcagcatc   1920

acaagtgact gaaattggct gtggatctgt tctttgtgaa agaattcctg atttctccat   1980

ggagcatgta cacaacaatt ttgatcatat taactgtact tcagttttgc attttattc    2040

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tttattctaa taacatgtat agatctaaag caggttgtgt tgtttacatg tttctacaca   2160

tttcatcctt taaaaagttg ttgagagagg ttgtatttac cttcccaagg ttggaaagca   2220

ggggaatttc ccagtgtcct agttttccac cagaggaata tgtgtaagta gcaaagtatt   2280

tgctgcttac atatagtgtg tatgtatgta tatatgtaaa ttgtgtgtta aagagctgat   2340

actgattttc atatgacaat gttaggcaaa ggcctccctg catttgaaga gcaggttttc   2400

atttatatgt atttttggga taaaaaaata aaatttgtaa atatagcccc caaaaaaaaa   2460

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                             2496
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<210> 24

<211> 1965

<212> DNA

<213> Unknown

<220>

<223> Clone S1+12-2 cDNA sequence

<400> 24

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tctcagaaga ggaccgcgga cttaaagcaa taaatgtaga tcttcaaagt gatgctgctc   120
tgcaggtgga catttctgat gctcttagtg agcgggataa agtaaaattc actgttcaca   180
caaagagttc attgccaaat tttaaacaaa acgagttttc agttgttcgg caacatgagg   240
aatttatctg gcttcatgat tcctttgttg aaaatgaaga ctatgcaggt tatatcattc   300
caccagcacc accaagacct gattttgatg cttcaaggga aaaactacag aagcttggtg   360
aaggagaagg gtcaatgacg aaggaagaat tcacaaagat gaaacaggaa ctggaagctg   420
aatatttggc aatattcaag aagacagttg cgatgcatga agtgttcctg tgtcgtgtgg   480
cagcacatcc tattttgaga agagatttaa atttccatgt cttcttggaa tataatcaag   540
atttgagtgt gcgaggaaaa aataaaaaag agaaacttga agacttcttt aaaaacatgg   600
ttaaatcagc agatggagta atcgtttcag gagtaaagga tgtagatgat ttctttgagc   660
acgaacgaac atttcttttg gagtatcata accgagttaa ggatgcatct gctaaatctg   720
atagaatgac aagatcccac aaaagtgctg cagatgatta caatagaatt ggttcttcat   780
tatatgcttt aggaactcag gattctacag atatatgcaa gttttttctc aaagtttcag   840
aactgttcga taaaacaaga aaaatagaag cacgagtgtc tgctgatgaa gacctcaaac   900
tttctgatct tttaaaatat tacttaagag aatctcaagc tgctaaggat ctcctgtatc   960
gaaggtctag gtcactagtg gattatgaaa atgctaataa agcactggat aaagcaagag  1020
caaaaaataa agatgttcta caggccgaaa cttcccaaca attatgttgt cagaaatttg  1080
aaaaaatatc tgagtctgca aaacaagaac ttatagattt taagacaaga agagttgctg  1140
cattcagaaa aaatttagtg gaactggcag agttagaact gaagcatgca aagggtaatc  1200
tacagttgct gcagaactgc ctggcagtgt aaatggaga cacataagcc acactccgcc  1260
ttcctgttaa aaagggctgc cttccttcaa attttatttt tgttttctta atgatgttaa  1320
gcatttatgc tcactggaaa caaacaaaaa gcagctgaaa aagtgcatca actcctcttt  1380
ttctgagaaa catggagcag cgcacgccca ggcgatgcca gtctgtgtgc cgtgatgccg  1440
cactgtgttc cccatgacag tggtccatca tcgtgcactc gtcatactca gaagtccaaa  1500
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gttcattctt ctttaaagta gcctctataa ctctgtttat tttataaata gtattcctta    1560

tggctgccac tcttatttac ctttaaataa tttctgaaat ttaacctttt cagaatgcat    1620

tgttgaaaca agataaagat tgcctttttt gaatttttta aattttgttt ttaaaagcat    1680

ataccacctt agttcattca tgtatcctgg taaagcatct taatcagact tatttttaat    1740

tactgaatat ttcttagacg ttttgggaca gattttatgt aatctttata agtatgattt    1800

ctgaagaaaa gcaaatgcat tagtatgttt gccttaaact tgtagactaa accaagtatt    1860

gtaaaataaa cagcgataac agtgatagtt tttaactcta tggtcattgt atcactctgg    1920

aaaatgtgga gtagctgtaa taaatctact cctgtattat gcttt                    1965
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<210> 25

<211> 2269

<212> DNA

<213> Unknown

<220>

<223> Clone S1+12-5 cDNA sequence

<400> 25

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gcggcgccga gtcccgggag cgcggtgggg gcagcgggcg cggggcgggc gcggggaccg     60

cgccagcctg tcactaatgt ctccctttgt gtctccccca tctcatcctt ttccccggcg    120

cgccgtgccc gccgacccca caggaaggcc tggacgacgg cccggacttc ctctcagaag    180

aggaccgcgg acttaaagca ataaatgtag atcttcaaag tgatgctgct ctgcaggtgg    240

acatttctga tgctcttagt gagcgggata aagtaaaatt cactgttcac acaaagagtt    300

cattgccaaa ttttaaacaa aacgagtttt cagttgttcg gcaacatgag gaatttatct    360

ggcttcatga ttcctttgtt gaaaatgaag actatgcagg ttatatcatt ccaccagcac    420

caccaagacc tgattttgat gcttcaaggg aaaaactaca gaagcttggt gaaggagaag    480

ggtcaatgac gaaggaagaa ttcacaaaga tgaaacagga actggaagcg ggttggataa    540

cagagaacct tgggtttatt ctactgctac ctccatcctc tgcatccttc ttttttgtct    600

tcactgaatg actaccctca cagagatcaa acttctccca tcattggtcc tgctggtttg    660

ctgtgaatat ttggcaatat tcaagaagac agttgcgatg catgaagtgt tcctgtgtcg    720

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tcaagatttg agtgtgcgag gaaaaaataa aaaagagaaa cttgaagact tctttaaaaa    840

catggttaaa tcagcagatg gagtaatcgt ttcaggagta aaggatgtag atgatttctt    900

tgagcacgaa cgaacatttc ttttggagta tcataaccga gttaaggatg catctgctaa    960
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atctgataga atgacaagat cccacaaaag tgctgcagat gattacaata gaattggttc    1020

ttcattatat gctttaggaa ctcaggattc tacagatata tgcaagtttt ttctcaaagt    1080

ttcagaactg ttcgataaaa caagaaaaat agaagcacga gtgtctgctg atgaagacct    1140

caaactttct gatcttttaa aatattactt aagagaatct caagctgcta aggatctcct    1200

gtatcgaagg tctaggtcac tagtggatta tgaaaatgct aataaagcac tggataaagc    1260

aagagcaaaa aataaagatg ttctacaggc cgaaacttcc caacaattat gttgtcagaa    1320

atttgaaaaa atatctgagt ctgcaaaaca agaacttata gattttaaga caagaagagt    1380

tgctgcattc agaaaaaatt tagtggaact ggcagagtta gaactgaagc atgcaaaggg    1440

taatctacag ttgctgcaga actgcctggc agtgttaaat ggagacacat aagccacact    1500

ccgccttcct gttaaaaagg gctgccttcc ttcaaatttt attttgttt tcttaatgat    1560

gttaagcatt tatgctcact ggaaacaaac aaaaagcagc tgaaaaagtg catcaactcc    1620

tcttttctg agaaacatgg agcagcgcac gcccaggcga tgccagtctg tgtgccgtga    1680

tgccgcactg tgttccccat gacagtggtc catcatcgtg cactcgtcat actcagaagt    1740

ccaaagttca ttcttcttta aagtagcctc tataactctg tttattttat aaatagtatt    1800

ccttatggct gccactctta tttacctta aataatttct gaaatttaac cttttcagaa    1860

tgcattgttg aaacaagata aagattgcct tttttgaatt ttttaaattt tgtttttaaa    1920

agcatatacc accttagttc attcatgtat cctggtaaag catcttaatc agacttattt    1980

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gatttctgaa gaaaagcaaa tgcattagta tgtttgcctt aaacttgtag actaaaccaa    2100

gtattgtaaa ataaacagcg ataacagtga tagtttttaa ctctatggtc attgtatcac    2160

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<210> 26

<211> 1834

<212> DNA

<213> Unknown

<220>

<223> clone S1+27 cDNA sequence

<400> 26
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gaaaataaga ttttatttta tcatccaaat gaggtagaaa agaatgagaa gattagaaat      240

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Page 31

<211> 2276

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<223> clone S1+28 cDNA sequence

<400> 27

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catacaccaa atgaaagaag atcaaagcaa aatccctgaa ggaatccaag ttgactctga     960

cgggctaatc accataacaa ctcccaataa acttgccacg ctcagtgttc gagccatgcc    1020

ccttccagaa gaagtcaccc agattctgga agaaaatagt gatttgattc gttctatgga    1080

gcagttgaca tcctctttga atgagggtga aaatactcac atgattcatc agaagaccca    1140

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agaagccagt agataccgag atttgggcaa tagcattgtg agtggcttcc aactagcaac    1380

cctctctggc cccatgtgtg aggagcctct catgggtgtc tgttttgttc tggaaaaatg    1440

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<212> PRT

<213> Unknown

<220>

<223> Starting sequence of SIP2

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